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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/847,809

DATE: 09/25/2001
TIME: 14:43:02

Input Set : N:\Crf3\RULE60\09847809.txt
Output Set: N:\CRF3\09252001\I847809.raw

SEQUENCE LISTING
C--> 5 (1) GENERAL INFORMATION:
      7   (i) APPLICANT: Bandman, Olga
      8   Hillman, Jennifer L.
      9   Lal, Preeti
     10   Corley, Neil C.
     11   Shah, Purvi
C--> 13   (ii) TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
     15   (iii) NUMBER OF SEQUENCES: 6
     17   (iv) CORRESPONDENCE ADDRESS:
     18   (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
     19   (B) STREET: 3174 Porter Drive
     20   (C) CITY: Palo Alto
     21   (D) STATE: CA
     22   (E) COUNTRY: USA
     23   (F) ZIP: 94304
     25   (v) COMPUTER READABLE FORM:
     26   (A) MEDIUM TYPE: Diskette
     27   (B) COMPUTER: IBM Compatible
     28   (C) OPERATING SYSTEM: DOS
     29   (D) SOFTWARE: FastSEQ for Windows Version 2.0
     31   (vi) CURRENT APPLICATION DATA:
C--> 32   (A) APPLICATION NUMBER: US/09/847,809
C--> 33   (B) FILING DATE: 01-May-2001
     34   (C) CLASSIFICATION:
     36   (vii) PRIOR APPLICATION DATA:
     37   (A) APPLICATION NUMBER: 09/270,270
     38   (B) FILING DATE: 1999-03-16
     40   (viii) ATTORNEY/AGENT INFORMATION:
     41   (A) NAME: Billings, Lucy J.
     42   (B) REGISTRATION NUMBER: 36,749
     43   (C) REFERENCE/DOCKET NUMBER: PF-0358 US
     45   (ix) TELECOMMUNICATION INFORMATION:
     46   (A) TELEPHONE: 650-855-0555
     47   (B) TELEFAX: 650-845-4166
     48   (C) TELEX:
     51 (2) INFORMATION FOR SEQ ID NO: 1:
     53   (i) SEQUENCE CHARACTERISTICS:
     54   (A) LENGTH: 328 amino acids
     55   (B) TYPE: amino acid
     56   (C) STRANDEDNESS: single
     57   (D) TOPOLOGY: linear
     59   (vii) IMMEDIATE SOURCE:
     60   (A) LIBRARY: RATRNOT02
     61   (B) CLONE: 922578
     63   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
     65 Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Leu Arg His

ENTERED

RAW SEQUENCE LISTING   DATE: 09/25/2001
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Input Set : N:\Crf3\RULE60\09847809.txt
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66    1               5                  10                 15
67    Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly
68                20                  25                 30
69    Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala
70            35                  40                 45
71    His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val
72        50                  55                 60
73    Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu
74    65              70                  75                 80
75    Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp
76                85                  90                 95
77    Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg
78                100                 105                110
79    His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp
80            115                 120                125
81    Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly
82        130             135                140
83    His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr
84    145             150                 155                160
85    Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp
86                165                 170                175
87    Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu
88            180                 185                190
89    His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr
90            195                 200                205
91    Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu
92        210             215                220
93    Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala
94    225             230                 235                240
95    Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn
96                245                 250                255
97    Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro
98            260                 265                270
99    Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu
100           275                 280                285
101   Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly
102       290             295                300
103   Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp
104   305             310                 315                320
105   Leu Thr Arg His His Asp Glu Leu
106                   325
108   (2) INFORMATION FOR SEQ ID NO: 2:
110        (i) SEQUENCE CHARACTERISTICS:
111            (A) LENGTH: 1463 base pairs
112            (B) TYPE: nucleic acid
113            (C) STRANDEDNESS: single
114            (D) TOPOLOGY: linear
116      (vii) IMMEDIATE SOURCE:
117            (A) LIBRARY: RATRNOT02
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RAW SEQUENCE LISTING   DATE: 09/25/2001
PATENT APPLICATION: US/09/847,809   TIME: 14:43:02

Input Set : N:\Crf3\RULE60\09847809.txt
Output Set: N:\CRF3\09252001\I847809.raw

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118          (B) CLONE: 922578
120     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
122  CGCAGAGCGG ACGTGGAGAG CGGACGNCAG CTGGATAACA GGGGACCGAT GATGTGGCGA     60
123  CCATCAGTTC TGCTGCTTCT GTTGCTACTG AGGCACGGGG CCCAGGGGAA GCCATCCCCA    120
124  GACGCAGGCC CTCATGGCCA GGGGAGGGTG CACCAGGCGG CCCCCCTGAG CGACGCTCCC    180
125  CATGATGACG CCCACGGGAA CTTCCAGTAC GACCATGAGG CTTTCCTGGG ACGGGAAGTG    240
126  GCCAAGGAAT TCGACCAACT CACCCCAGAG GAAAGCCAGG CCCGTCTGGG GCGGATCGTG    300
127  GACCGCATGG ACCGCGCGGG GGACGGCGAC GGCTGGGTGT CGCTGGCCGA GCTTCGCGCG    360
128  TGGATCGCGC ACACGCAGCA GCGGCACATA CGGGACTCGG TGAGCGCGGC CTGGGACACG    420
129  TACGACACGG ACCGCGACGG GCGTGTGGGT TGGGAGGAGC TGCGCAACGC CACCTATGGC    480
130  CACTACGCGC CCGGTGAAGA ATTTCATGAC GTGGAGGATG CAGAGACCTA CAAAAAGATG    540
131  CTGGCTCGGG ACGAGCGGCG TTTCCGGGTG GCCGACCAGG ATGGGGACTC GATGGCCACT    600
132  CGAGAGGAGC TGACAGCCTT CCTGCACCCC GAGGAGTTCC CTCACATGCG GGACATCGTG    660
133  ATTGCTGAAA CCCTGGAGGA CCTGGACAGA AACAAAGATG GCTATGTCCA GGTGGAGGAG    720
134  TACATCGCGG ATCTGTACTC AGCCGAGCCT GGGGAGGAGG AGCCGGCGTG GGTGCAGACG    780
135  GAGAGGCAGC AGTTCCGGGA CTTCCGGGAT CTGAACAAGG ATGGGCACCT GGATGGGAGT    840
136  GAGGTGGGCC ACTGGGTGCT GCCCCCTGCC CAGGACCAGC CCCTGGTGGA AGCCAACCAC    900
137  CTGCTGCACG AGAGCGACAC GGACAAGGAT GGGCGGCTGA GCAAAGCGGA AATCCTGGGT    960
138  AATTGGAACA TGTTTGTGGG CAGTCAGGCC ACCAACTATG GCGAGGACCT GACCCGGCAC   1020
139  CACGATGAGC TGTGAGCACC GCGCACCTGC CACAGCCTCA GAGGCCCGCA CAATGACCGG   1080
140  AGGAGGGGCC GCTGTGGTCT GGCCCCCTCC CTGTCCAGGC CCCGCAGGAG GCAGATGCAG   1140
141  TCCCAGGCAT CCTCCTGCCC CTGGGCTCTC AGGGACCCCC TGGGTCGGCT TCTGTCCCTG   1200
142  TCACACCCCC AACCCCAGGG AGGGGCTGTC ATAGTCCCAG AGGATAAGCA ATACCTATTT   1260
143  CTGACTGAGT CTCCCAGCCC AGACCCAGGG ACCCTTGGCC CCAAGCTCAG CTCTAAGAAC   1320
144  CGCCCCAACC CCTCCAGCTC CAAATCTGAG CCTCCACCAC ATAGACTGAA ACTCCCCTGG   1380
145  CCCCAGCCCT CTCCTGCCTG GCCTGGCCTG GGACACCTCC TCTCTGCCAG GAGGCAATAA   1440
146  AAGCCAGCGC CGGGAAAAAA AAA                                           1463
148  (2) INFORMATION FOR SEQ ID NO: 3:
150      (i) SEQUENCE CHARACTERISTICS:
151          (A) LENGTH: 315 amino acids
152          (B) TYPE: amino acid
153          (C) STRANDEDNESS: single
154          (D) TOPOLOGY: linear
156     (vii) IMMEDIATE SOURCE:
157          (A) LIBRARY: BLADNOT03
158          (B) CLONE: 1601793  .
160      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
162  Met Asp Leu Arg Gln Phe Leu Met Cys Leu Ser Leu Cys Thr Ala Phe
163   1               5                  10                  15
164  Ala Leu Ser Lys Pro Thr Glu Lys Lys Asp Arg Val His His Glu Pro
165              20                  25                  30
166  Gln Leu Ser Asp Lys Val His Asn Asp Ala Gln Ser Phe Asp Tyr Asp
167          35                  40                  45
168  His Asp Ala Phe Leu Gly Ala Glu Glu Ala Lys Thr Phe Asp Gln Leu
169      50                  55                  60
170  Thr Pro Glu Glu Ser Lys Glu Arg Leu Gly Lys Ile Val Ser Lys Ile
171  65                  70                  75                  80
172  Asp Gly Asp Lys Asp Gly Phe Val Thr Val Asp Glu Leu Lys Asp Trp
173              85                  90                  95
```

```
174  Ile Lys Phe Ala Gln Lys Arg Trp Ile Tyr Glu Asp Val Glu Arg Gln
175              100             105             110
176  Trp Lys Gly His Asp Leu Asn Glu Asp Gly Leu Val Ser Trp Glu Glu
177          115             120             125
178  Tyr Lys Asn Ala Thr Tyr Gly Tyr Val Leu Asp Asp Pro Asp Pro Asp
179      130             135             140
180  Asp Gly Phe Asn Tyr Lys Gln Met Met Val Arg Asp Glu Arg Arg Phe
181  145             150             155             160
182  Lys Met Ala Asp Lys Asp Gly Asp Leu Ile Ala Thr Lys Glu Glu Phe
183              165             170             175
185  Thr Ala Phe Leu His Pro Glu Glu Tyr Asp Tyr Met Lys Asp Ile Val
186          180             185             190
187  Val Gln Glu Thr Met Glu Asp Ile Asp Lys Asn Ala Asp Gly Phe Ile
188          195             200             205
189  Asp Leu Glu Glu Tyr Ile Gly Asp Met Tyr Ser His Asp Gly Asn Thr
190      210             215             220
191  Asp Glu Pro Glu Trp Val Lys Thr Glu Arg Glu Gln Phe Val Glu Phe
192  225             230             235             240
193  Arg Asp Lys Asn Arg Asp Gly Lys Met Asp Lys Glu Glu Thr Lys Asp
194              245             250             255
195  Trp Ile Leu Pro Ser Asp Tyr Asp His Ala Glu Ala Glu Ala Arg His
196          260             265             270
197  Leu Val Tyr Glu Ser Asp Gln Asn Lys Asp Gly Lys Leu Thr Lys Glu
198          275             280             285
199  Glu Ile Val Asp Lys Tyr Asp Leu Phe Val Gly Ser Gln Ala Thr Asp
200      290             295             300
201  Phe Gly Glu Ala Leu Val Arg His Asp Glu Phe
202  305             310             315
204  (2) INFORMATION FOR SEQ ID NO: 4:
206      (i) SEQUENCE CHARACTERISTICS:
207          (A) LENGTH: 2658 base pairs
208          (B) TYPE: nucleic acid
209          (C) STRANDEDNESS: single
210          (D) TOPOLOGY: linear
212      (vii) IMMEDIATE SOURCE:
213          (A) LIBRARY: BLADNOT03
214          (B) CLONE: 1601793
216      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
218  CCCGCTTCCG GTTGGGCGGT GCTTGCGCGC GTGAGCTGAG CCGGTGGGTG AGCGGCGGCC    60
219  ACGGCATCCT GTGCTGTGGG GGCTACGAGG AAAGATCTAA TTATCATGGA CCTGCGACAG   120
220  TTTCTTATGT GCCTGTCCCT GTGCACAGCC TTTGCCTTGA GCAAACCCAC AGAAAAGAAG   180
221  GACCGTGTAC ATCATGAGCC TCAGCTCAGT GACAAGGTTC ACAATGATGC TCAGAGTTTT   240
222  GATTATGACC ATGATGCCTT CTTGGGTGCT GAAGAAGCAA AGACCTTTGA TCAGCTGACA   300
223  CCAGAAGAGA GCAAGGAAAG GCTTGGAAAG ATTGTAAGTA AAATAGATGG CGACAAGGAC   360
224  GGGTTTGTCA CTGTGGATGA GCTCAAAGAC TGGATTAAAT TTGCACAAAA GCGCTGGATT   420
225  TACGAGGATG TAGAGCGACA GTGGAAGGGG CATGACCTCA ATGAGGACGG CCTCGTTTCC   480
226  TGGGAGGAGT ATAAAAATGC CACCTACGGC TACGTTTTAG ATGATCCAGA TCCTGATGAT   540
227  GGATTAAACT ATAAACAGAT GATGGTTAGA GATGAGCGGA GGTTTAAAAT GGCAGACAAG   600
228  GATGGAGACC TCATTGCCAC CAAGGAGGAG TTCACAGCTT CCTGCACCC TGAGGAGTAT   660
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229  GACTACATGA AAGATATAGT AGTACAGGAA ACAATGGAAG ATATAGATAA GAATGCTGAT   720
230  GGTTTCATTG ATCTAGAAGA GTATATTGGT GACATGTACA GCCATGATGG GAATACTGAT   780
231  GAGCCAGAAT GGGTAAAGAC AGAGCGAGAG CAGTTTGTTG AGTTTCGGGA TAAGAACCGT   840
232  GATGGGAAGA TGGACAAGGA AGAGACCAAA GACTGGATCC TTCCCTCAGA CTATGATCAT   900
233  GCAGAGGCAG AAGCCAGGCA CCTGGTCTAT GAATCAGACC AAAACAAGGA TGGCAAGCTT   960
234  ACCAAGGAGG AGATCGTTGA CAAGTATGAC TTATTTGTTG GCAGCCAGGC CACAGATTTT  1020
235  GGGGAGGCCT TAGTACGGCA TGATGAGTTC TGAGCTACGG AGGAACCCTC ATTTCCTCAA  1080
236  AAGTAATTTA TTTTTACAGC TTCTGGTTTC ACATGAAATT GTTTGCGCTA CTGAGACTGT  1140
237  TACTACAAAC TTTTTAAGAC ATGAAAAGGC GTAATGAAAA CCATCCCGTC CCCATTCCTC  1200
238  CTCCTCTCTG AGGGACTGGA GGGAAGCCGT GCTTCTGAGG AACAACTCTA ATTAGTACAC  1260
239  TTGTGTTTGT AGATTTACAC TTTGTATTAT GTATTAACAT GGCGTGTTTA TTTTTGTATT  1320
240  TTTCTCTGGT TGGGAGTATG ATATGAAGGA TCAAGATCCT CAACTCACAC ATGTAGACAA  1380
241  ACATTAGCTC TTTACTCTTT CTCAACCCCT TTTATGATTT TAATAATTCT CACTTAACTA  1440
242  ATTTTGTAAG CCTGAGATCA ATAAGAAATG TTCAGGAGAG AGGAAAGAAA AAAAATATAT  1500
243  GCTCCACAAT TTATATTTAG AGAGAGAACA CTTAGTCTTG CCTGTCAAAA AGTCCAACAT  1560
244  TTCATAGGTA GTAGGGGCCA CATATTACAT TCAGTTGCTA TAGGTCCAGC AACTGAACCT  1620
245  GCCATTACCT GGGCAAGGAA AGATCCCTTT GCTCTAGGAA AGCTTGGCCC AAATTGATTT  1680
246  TCTTCTTTTT CCCCCTGTAG GACTGACTGT TGGCTAATTT TGTCAAGCAC AGCTGTGGTG  1740
247  GGAAGAGTTA GGGCCAGTGT CTTGAAAATC AATCAAGTAG TGAATGTGAT CTCTTTGCAG  1800
248  AGCTATAGAT AGAAACAGCT GGAAAACTAA AGGAAAAATA CAAATGTTTT CGGGGCATAC  1860
249  ATTTTTTTTC TGGGTGTGCA TCTGTTGAAA TGCTCAAGAC TTAATTATTT GCCTTTTGAA  1920
250  ATCACTGTAA ATGCCCCCAT CCGGTTCCTC TTCTTCCCAG GTGTGCCAAG GAATTAATCT  1980
251  TGGTTTCACT ACAATTAAAA TTCACTCCTT TCCAATCATG TCATTGAAAG TGCCTTTAAC  2040
252  GAAAGAAATG GTCACTGAAT GGGAATTCTC TTAAGAAACC CTGAGATTAA AAAAAGACTA  2100
253  TTTGGATAAC TTATAGGAAA GCCTAGAACC TCCCAGTAGA GTGGGGATTT TTTTCTTCTT  2160
254  CCCTTTCTCT TTTGGACAAT AGTTAAATTA GCAGTATTAG TTATGAGTTT GGTTGCAGTG  2220
255  TTCTTATCTT GTGGGCTGAT TTCCAAAAAC CACATGCTGC TGAATTTACC AGGGATCCTC  2280
256  ATACCTCACA ATGCAAACCA CTTACTACCA GGCCTTTTTC TGTGTCCACT GGAGAGCTTG  2340
257  AGCTCACACT CAAAGATCAG AGGACCTACA GAGAGGGCTC TTTGGTTTGA GGACCATGGC  2400
258  TTACCTTTCC TGCCTTTGAC CCATCACACC CCATTTCCTC CTCTTTCCCT CTCCCCGCTG  2460
259  CCAAAAAAAA AAAAAAAGGA AACGTTTATC ATGAATCAAC AGGGTTTCAG TCCTTATCAA  2520
260  AGAGAGATGT GGAAAGAGCT AAAGAAACCA CCCTTTGTTC CCAACTCCAC TTTACCCATA  2580
261  TTTTATGCAA CACAAACACT GTCCTTTTGG GTCCCTTTCT TACAGATGGG ACCTCTTGAG  2640
262  GAAGGAATTA TCGTATTC                                                2658
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264 (2) INFORMATION FOR SEQ ID NO: 5:
266   (i) SEQUENCE CHARACTERISTICS:
267   (A) LENGTH: 331 amino acids
268   (B) TYPE: amino acid
269   (C) STRANDEDNESS: single
270   (D) TOPOLOGY: linear
272   (vii) IMMEDIATE SOURCE:
273   (A) LIBRARY: GenBank
274   (B) CLONE: 1262329
276   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
278 Met Ala Arg Gly Gly Arg Gly Arg Arg Leu Gly Leu Ala Leu Gly Leu
279 1   5   10   15
280 Leu Leu Ala Leu Val Leu Ala Pro Arg Val Leu Arg Ala Lys Pro Thr
281   20   25   30
282 Val Arg Lys Glu Arg Val Val Arg Pro Asp Ser Glu Leu Gly Glu Arg

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/847,809

DATE: 09/25/2001
TIME: 14:43:03

Input Set : **N:\Crf3\RULE60\09847809.txt**
Output Set: **N:\CRF3\09252001\I847809.raw**

L:5 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
L:13 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]
L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]